

AMENDMENT

In the Claims:

Please amend claims 1, 9, 19-22, 24 and 25 as follows:

1. [TWICE AMENDED] A method of making a mixture of VNTR alleles

and their flanking regions of the genomic DNA of one or more members of a species of interest, which method comprises the steps of:

- a) dividing genomic DNA of the species of interest into fragments,
- b) ligating to each end of each fragment an adaptor thereby forming a mixture of adaptor-terminated fragments in which each 3'-end is blocked to prevent enzymatic chain extension,
- c) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR primer wherein said portion of the mixture of adaptor-terminated fragments serves as a template to create a mixture of 5'-flanking VNTR amplimers;
- d) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR antisense primer wherein said portion of the mixture of adaptor-terminated fragments serves as template to create a mixture of 3'-flanking VNTR amplimers,
- e) and producing a desired mixture of VNTR alleles and their flanking regions by contacting genomic DNA of the one or more members of the species of interest with the mixture of 5'-flanking VNTR amplimers and/or the mixture of 3'-flanking VNTR amplifiers as primers wherein said genomic DNA of the one or more members of the species of interest is used as template.

Q3
Sub 1

9. [TWICE AMENDED] The method of claim 6, wherein at least one VNTR allele and its flanking sequences representative of those which manifest the trait of interest, is hybridised with a mixture of VNTR alleles and their flanking sequences representative of alleles which do not manifest the trait of interest, and at least one match and/or at least one mis-match is selected to provide at least one VNTR allele or fragment thereof which is characteristic of the trait of interest.

Q3
Sub 1

19. [TWICE AMENDED] The method of claim 17, wherein at least one VNTR allele and its flanking sequence representative of alleles which manifest the trait of interest, is hybridised with a mixture of VNTR alleles and their flanking sequences representative of those which do not manifest the trait of interest, and at least one match and/or at least one mis-match is selected to provide at least one VNTR allele or fragment thereof which is characteristic of the trait of interest.

Q4
Sub 1

20. [AMENDED] The method of claim 19, wherein the at least one VNTR allele and its flanking sequence representative of alleles which manifest the trait of interest, is provided with 3'-overlapping ends.

Q5
Sub 1
D2

21. [TWICE AMENDED] A method of making a mixture of amplimers which method comprises the steps of:

- a) dividing genomic DNA of one or more members of a species of interest into fragments,

(S 5' cont'd)

S 13' 1 cont'd

b) ligating to each end of each fragment an adaptor thereby forming a mixture of adaptor-terminated fragments in which each 3'-end is blocked to prevent enzymatic chain extension, and

c) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR primer wherein said portion of the mixture of adaptor-terminated fragments serves as a template to create a mixture of 5'-flanking VNTR amplimers, and/or

d) a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR antisense primer wherein said portion of the mixture of adaptor-terminated fragments serves as a template to create a mixture of 3'-flanking VNTR amplimers.

(S 10)

S 10

D

22. [AMENDED] A method of identifying an allele which is linked to a trait of interest, which method comprises incubating together under hybridisation conditions: at least one molecule of nucleic acid containing a polymorphic allele and its flanking sequences representative of alleles which manifest the trait of interest; and a mixture of molecules of nucleic acid which contain polymorphic alleles and their flanking sequences representative of those which do not manifest the trait of interest; and selecting at least one match and/or at least one mis-match to provide at least one allele or fragment thereof which is linked to the trait of interest.

R S 13'

24. [AMENDED] The method of claim 22, wherein the at least one allele and its flanking sequences representative of alleles which manifest the trait of interest, is provided with 3'-overlapping ends.